IN THE CLAIMS:

Claims 2, 11, and 16 were previously canceled without prejudice or disclaimer. Claims 1, 3, 6, 10, 12, 17, and 22 have been amended herein without prejudice or disclaimer. All of the pending claims 1, 3-10, 12-15, and 17-22 are presented below. This listing of claims will replace all prior versions and listings of claims in the application. Please enter these claims as amended.

Listing of the Claims:

1. (Currently amended) A genetically transformed plant, comprising:

~~a means for modulating mitochondrially generated acetyl-CoA and/or respiration rate in the genetically transformed plant as compared to a genomically unmodified plant of the same genotype wherein the means for modulating mitochondrially generated acetyl-CoA and/or respiration rate is~~ an isolated nucleic acid sequence ~~incorporated~~ transformed into the plant's genome having a sequence selected from the group of sequences consisting of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3 and SEQ ID NO:4; and

a promoter operatively linked to the ~~means for modulating mitochondrially generated acetyl-CoA and/or respiration rate~~ nucleic acid sequence transformed into the plant's genome.

2.(Canceled)

3. (Currently amended) The genetically transformed plant of claim 1, wherein the plant is selected from the group consisting of ~~borage, Canola, castor, cocoa bean, corn, cotton, *Crambe* spp., *Cuphea* spp., flax, *Lesquerella* and *Limnanthes* spp., Linola, nasturtium, *Oenothera* spp., olive, palm, peanut, rapeseed, safflower, soybean, sunflower, tobacco, *Vernonia* spp., wheat, barley, rice, oat, sorghum, rye, and other~~ members of the *Gramineae*.

4. (Original) The genetically transformed plant of claim 3, wherein the plant is Canola.

5. (Previously presented) The genetically transformed plant of claim 1, wherein the

means for modulating mitochondrially generated acetyl-CoA and/or respiration rate further includes a gene encoding a pyruvate dehydrogenase kinase oriented in an anti-sense direction.

6. (Currently amended) The genetically transformed plant of claim 1, wherein the promoter is an ubiquitin gene promoter.

7. (Original) The genetically transformed plant of claim 1, wherein the promoter is a phaseolin promoter.

8. (Previously presented) A process for modulating mitochondrially generated acetyl-CoA and/or respiration rate in a transgenic plant, the process comprising:
cloning a gene encoding a *Brassica* pyruvate dehydrogenase kinase protein into a vector, wherein the gene comprises a sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3 and SEQ ID NO:4;
positioning the gene in an anti-sense orientation within the vector; and
transforming a plant with the vector to produce the transgenic plant.

9. (Original) The process according to claim 8, further comprising:
linking a promoter to the gene.

10. (Currently amended) The process according to claim 9, wherein the promoter is an ubiquitin gene promoter or a phaseolin promoter.

11. (Canceled)

12. (Currently amended) The process according to claim 8, wherein the plant is selected from the group consisting of ~~borage, Canola, castor, cocoa bean, corn, cotton, *Crambe* spp., *Cuphea* spp., flax, *Lesquerella* and *Limnanthes* spp., Linola, nasturtium, *Oenothera* spp., olive, palm, peanut, rapeseed, safflower, soybean, sunflower, tobacco, *Vernonia* spp., wheat, barley,~~

~~rice, oat, sorghum, rye, and other~~ members of the *Gramineae*.

13. (Original) The process according to claim 12, wherein the plant is Canola.

14. (Original) A transgenic plant obtained by the process according to claim 8.

15. (Previously presented) A process for modulating mitochondrially generated acetyl-CoA and/or respiration rate in a transgenic plant, the process comprising:
cloning a gene encoding a *Brassica* pyruvate dehydrogenase kinase protein into a vector, wherein the gene comprises a sequence selected from the group of sequences consisting of SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3 and SEQ ID NO:4;
transforming the vector into a plant to produce the transgenic plant; and
reducing production of the *Brassica* pyruvate dehydrogenase kinase protein in the transgenic plant.

16. (Canceled)

17. (Currently amended) The process according to claim 15, wherein the plant is selected from the group consisting of ~~borage, Canola, castor, cocoa bean, corn, cotton, *Crambe* spp., *Cuphea* spp., flax, *Lesquerella* and *Limnanthes* spp., Linola, nasturtium, *Oenothera* spp., olive, palm, peanut, rapeseed, safflower, soybean, sunflower, tobacco, *Vernonia* spp., wheat, barley, rice, oat, sorghum, rye, and other~~ members of the *Gramineae*.

18. (Original) The process according to claim 17, wherein the plant is Canola.

19. (Original) The process according to claim 15, wherein the step for reducing production of the *Brassica* pyruvate dehydrogenase kinase protein comprises positioning the gene encoding the *Brassica* pyruvate dehydrogenase kinase protein in an anti-sense orientation in the vector.

20. (Previously presented) A transgenic plant produced by the process according to claim 15.

21. (Previously presented) A combination of DNA fragments comprising SEQ ID NO:1, SEQ ID NO:2, SEQ ID NO:3 and SEQ ID NO:4.

22. (Currently amended) A genetically transformed plant, comprising:

~~a means for modulating mitochondrially generated acetyl CoA and/or respiration rate in the genetically transformed plant as compared to a genomically unmodified plant of the same genotype wherein the means for modulating mitochondrially generated acetyl CoA and/or respiration rate is~~ an isolated nucleic acid ~~incorporated~~ transformed into the plant's genome having a sequence of SEQ ID NO:1; and

a promoter operatively linked to the ~~means for modulating mitochondrially generated acetyl CoA and/or respiration rate~~ isolated nucleic acid transformed into the plant's genome.